



FIG. 1A

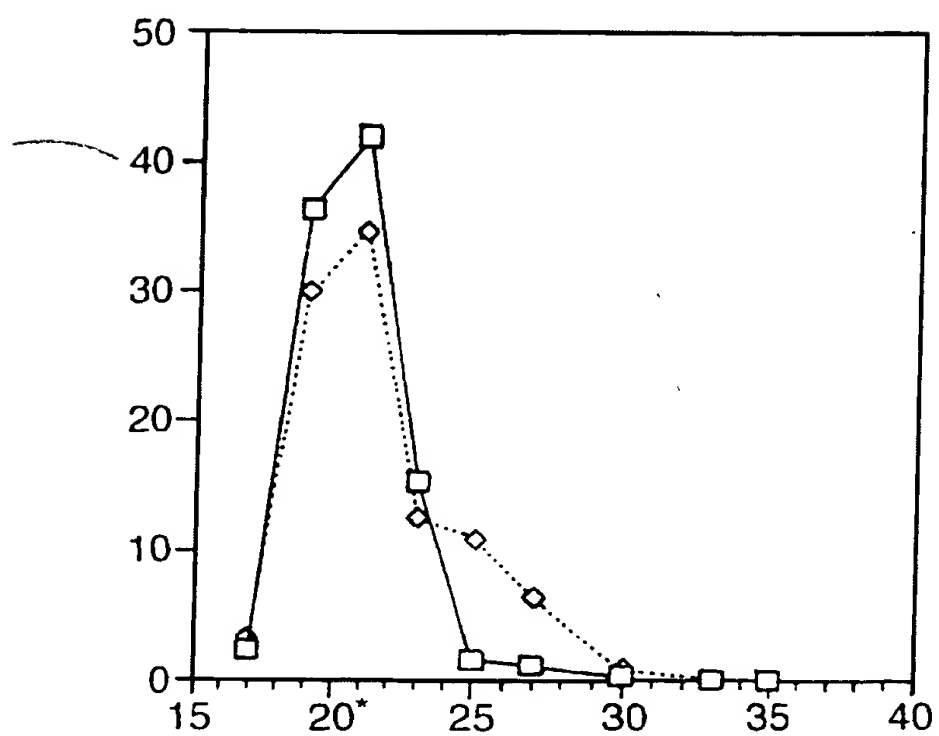
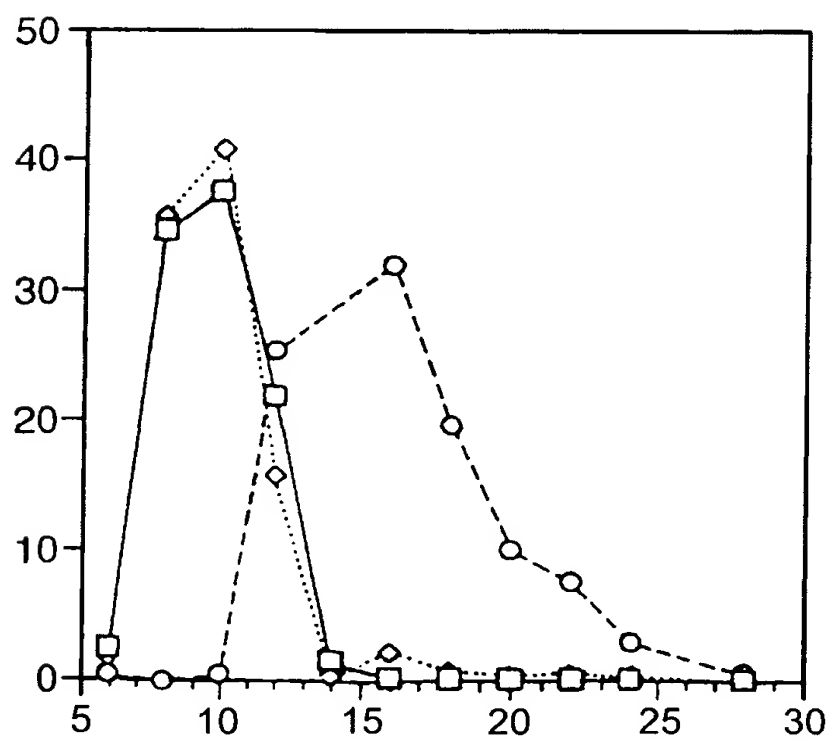
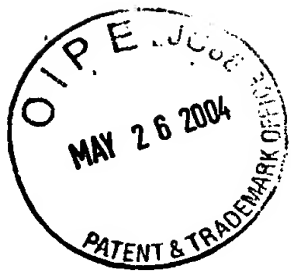


FIG. 1B





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sclig4 1 MISALDSIPEQNFAPSPDFKWLCEELFVKIHEVQINGTAGTKSRSEFKYYEIIISNFVEMWRKTVGNNIYPADVIALPYEDRRIRINIKDYVLIIRTICSYKLPKNSATEQORNDWKQRVG
hligivMRIIPQLEERERMAVGIKETMAKLKYLIELLNLPRDGKDALKLNRYRTPTE

sclig4 121 KGNLSSLLVEE..IAKRRAPSSKAITDNVNNHYLDSLGDRAFGRCGRFSLVRSKPFHHCVENNSFVELRYFFDIVLKNRVIGGOEHKLNCWHPDAQDYLSVSDIKVVTSKYVDEK
hligiv 51 THGDAGDFAMIAFYVLKPRCLQKG.SLTIQQVNDLLDSIASNNSAKR...KOLIK.KSLIQLITQSSALEQKWLIRMIKOLKLGVSQQTIFSVFHNDAEALHNVTDLIEKVCRCQLEHDS

sclig4 239 VRDKDDLSIKVGFAPQAKKVNLSYEKICRTL.HDDFLVEEKDGERIQVHYMNYGESIKFESRRCIDYLYGASLSSETISQHLR...FTDSVKECVIDGEMVTFDAKRRVILPFG
hligiv 166 VGL..SDISITLFSASKPMALAIADI..EHIEKDMKHQSEYIETKLDGERMQH..KGDVYKYESRNGYNYDQFGASPTGSLTPFIHNAEKADIQICILDGEMMAYNPNITQTFMQG

sclig4 356 LVKGSAAKALSFNINNVDFHPLAVEDLIVLNGTSLTPLPHQRKOYVNSILSELKNIVEIVRSRRCYGVESIKKSLEVAISLGSSEGVLYKYNSSYNVASRNNNWKVKPEVLEEFGE
hligiv 280 TKFDIKRM.....VEDSDLOTCYCVEDVLMVNNKOLCHETLRKRYEILSSIFTPIPGRIEIVQTOAHTKNEVIDALNEADKREEGIMVKQPLSIYKPKDKRGEGLKIKPEVVSGLMD

sclig4 476 NDDLIVIG..RDSKKDSFMLGLVLDDEEYKXHQDSSEITVDHSSQEKHIQNSRRRVKILSFCSIANCISQEEFKEIDRTRGHWRRTSEVAPPASILEFGSKIPAEWIDPSESIVLE
hligiv 394 EDDLIVGGYWGKSRGGMSHFLCAVAE..KPPPEKPSVFH.....TLSRVGSCTMKELYDLGLKAKYMKPFHRKAPPSIL.CGTEKEEVVIEPCNSVIVQ

sclig4 594 IKRSILDNTE TNMQYATNCTLYGGYCKRIRYDKEMWDCYTNLNDLYESRTVKS.....NPSYQAEERSQLGLTRKRRKRVLISDSFHQNRKQL.PI SNIFAGLLEFVLSDYVTED
hligiv 492 IKAAEIVPSD...MYKTGCTLRFPRIEKIRDDKEMHECMTLDDLEQLRGKASGLASKHLYIGGDDEPQEKKRKAAPKMKVIGIIEHLKAPNL TNVNKISNIFEDVEFCVMSCTDSQ.

sclig4 702 TGI RITRAEIEKTI VEHGCKLIYNVILKRHSIGDVRLISCKTTTECKALJ.DRGYDILHNNVVIDCIAYKRLILIEPNYCNVSQKRAVAEKRVDCLGDSFENDISETKLSLYKSQLS
hligiv 607PKPDLENRIAEFGG.....YIVQNPQPDYTCVLAGSENIRVKNIIILSNKHVVKEAMLECFKTKSFVPWQPRFMHMCPSYKEHFAREYDCYGDYFIDTDLNQLKEVFTSGIKN

sclig4 821 LPPMGELEIDSEVRRF.....PFLFESNRIAVPR.....RKISTEDDIEMKTKLFGGKITDQOSLCNLIIPYTDPILRKDCMNEVHEKIKEQIKASDTIPKIA RVVAPPEWVDS
hligiv 717 SNEQTPEEASLIADLEYRYSWDCSPLSMERHRTVLD SYAVINDLSTKNEGTRLAIKALELRFHGAK.....VVSCLAEGVSHVIGEDHSRVADFKAFRRJFKRKFKILKESWVTD

sclig4 928 INENCQVPEEDFFVVNY*
hligiv 831 I.DKCELOEENQYLI*

FIG. 2



FIG. 3A

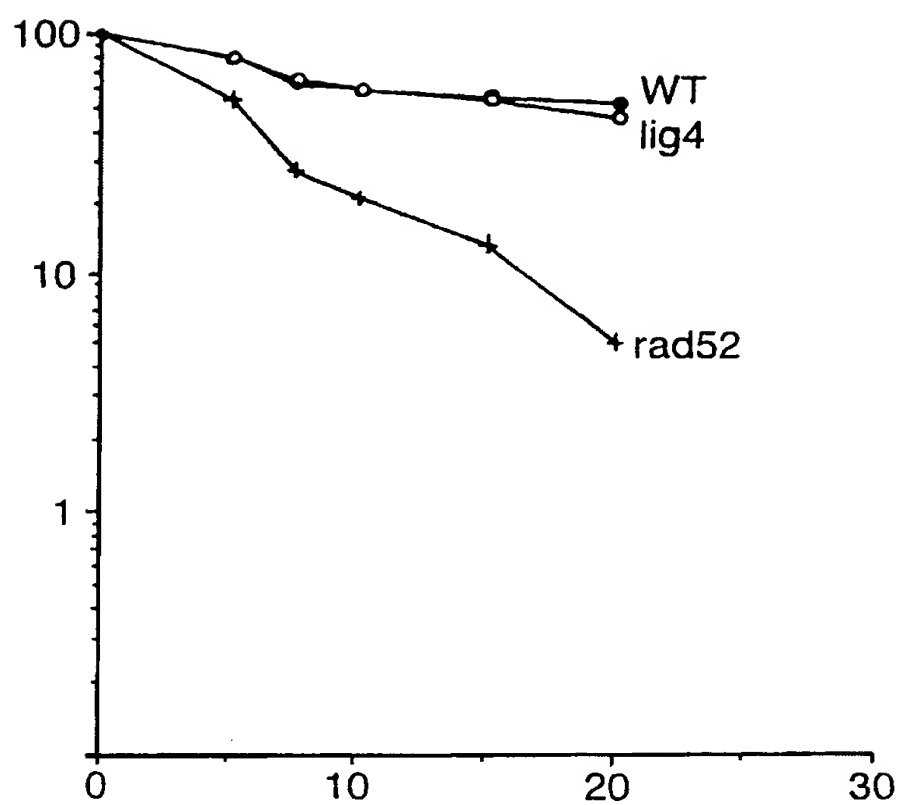


FIG. 3B

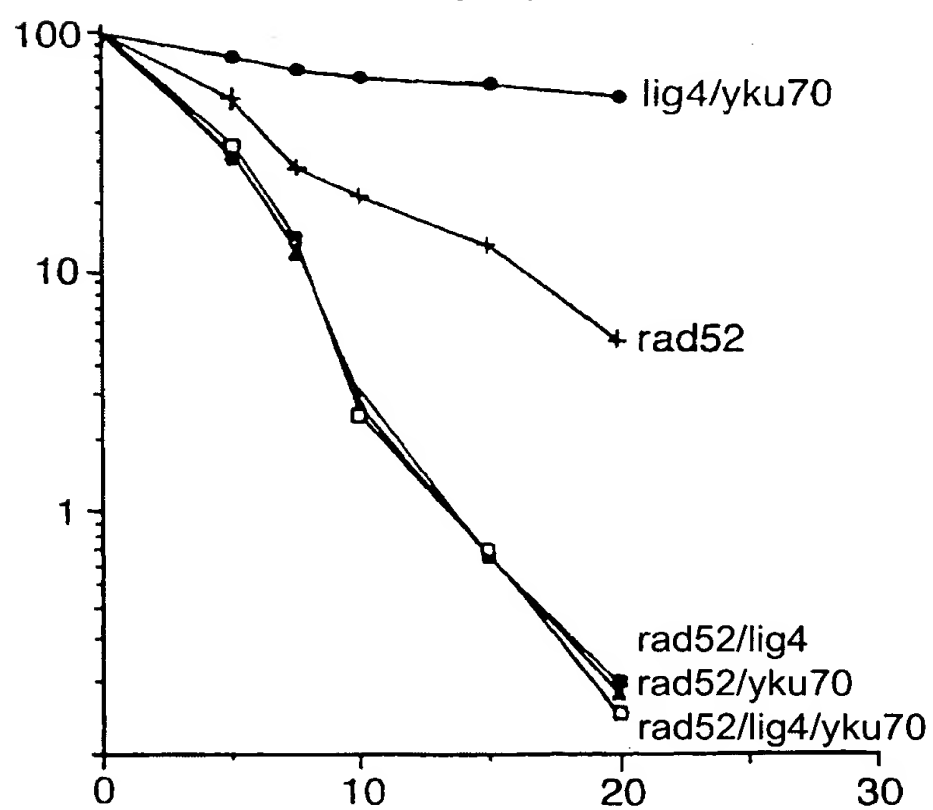




FIG. 4

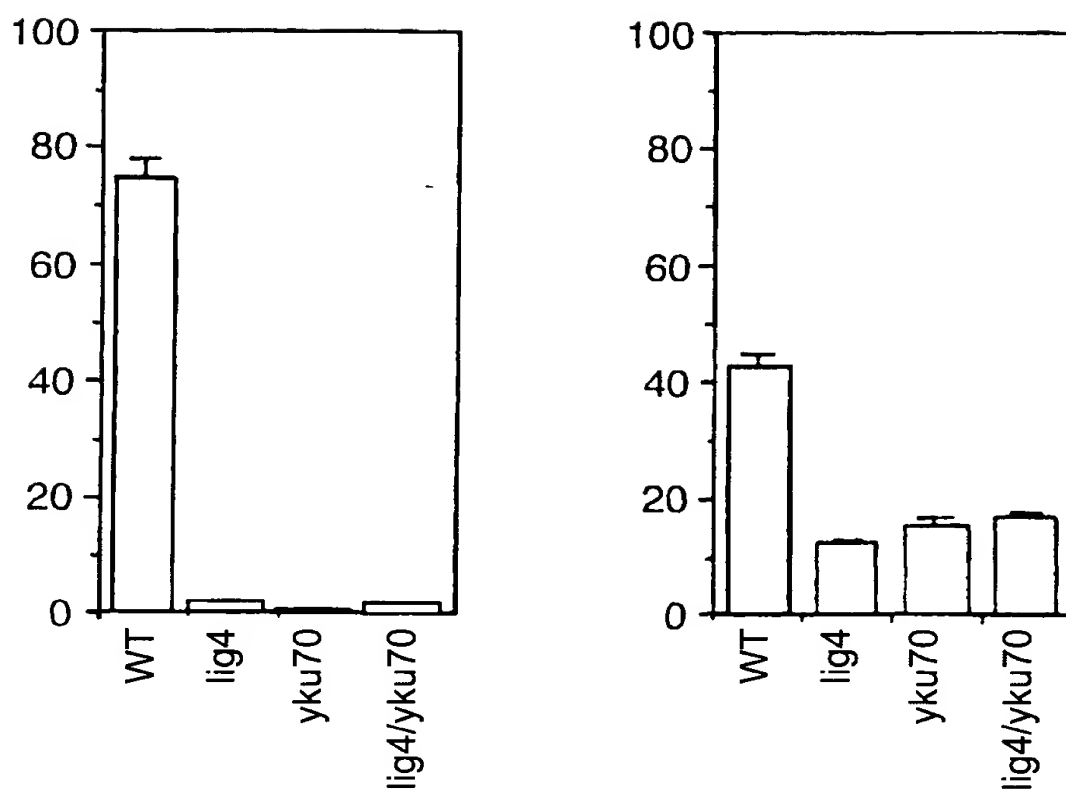
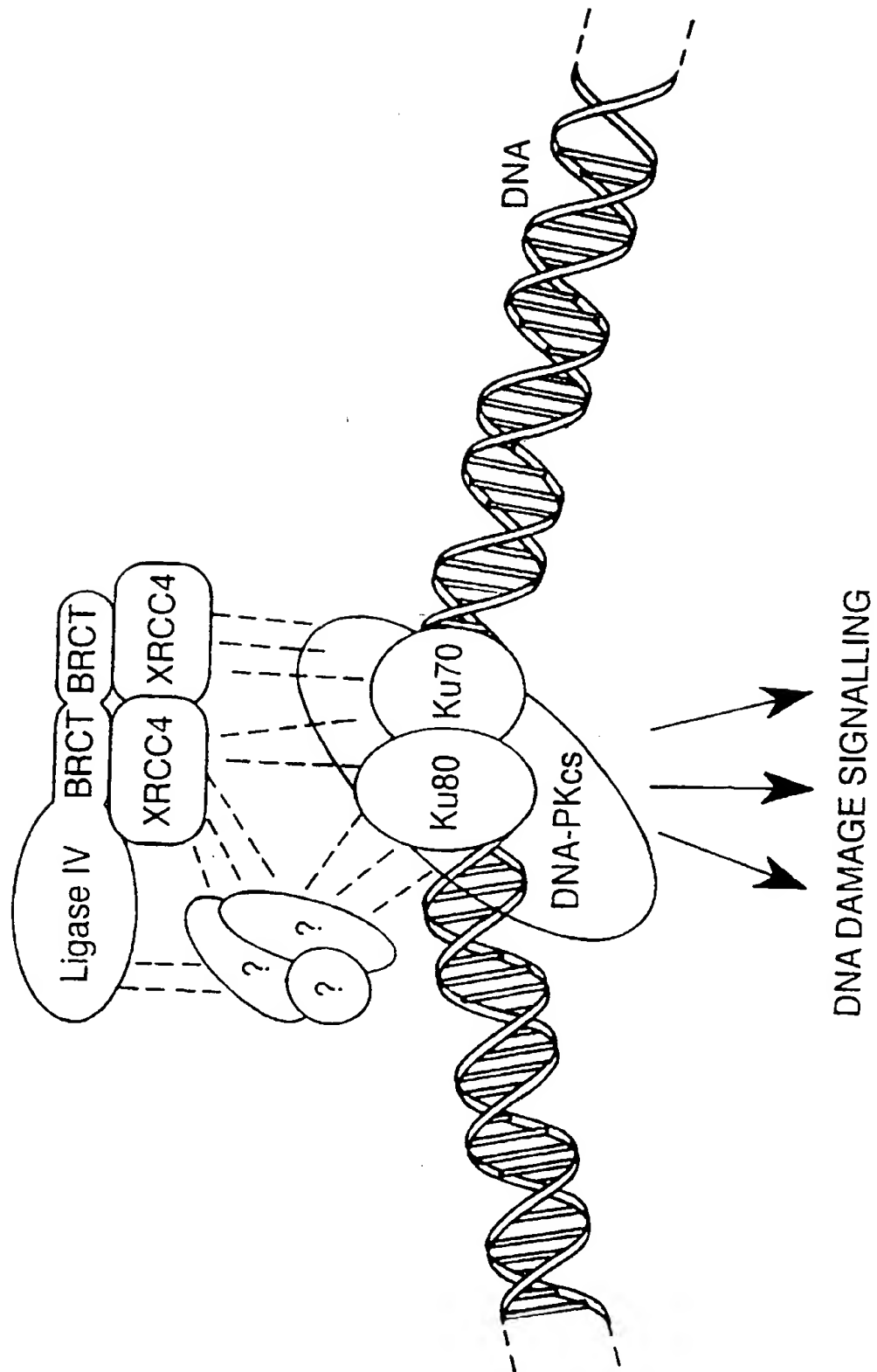


FIG. 5





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FIG. 6

GTGATTAAATAGGCTGAAATCAGTGTTTAGTAACTACGTACGTTGTACATGTAACATTGT
1 -----+-----+-----+-----+-----+-----+-----+ 60
CACTAATTTATCCGACTTTAGTCACAAATCATTTGATGCATGCAACATGTACATTGTAACA
V I K * A E I S V * * L R T L Y M * H C -
GATATAAATCGTAAGATTCGCCGAGTATAGATCAATAATATCGGTTTCATCACTTACGTT
61 -----+-----+-----+-----+-----+-----+-----+ 120
CTATATTTAGCATTCTAAGCGGCTCATATCTAGTTATTATAGCCAAAGTAGTGAATGCAA
D I N R K I R R V * I N N I G F I T Y V -
GTTTGTGCAGTACTAGAGTTAAGATCGTTTTGATCCCTTATTTTCTTCTTTTTCCTTT
121 -----+-----+-----+-----+-----+-----+-----+ 180
CAAACACGTCATGATCTCAATTCTAGCAAAAGCTAGGGAATAAAAGAAGAAAAAAGGAAA
V C A V L E L R S F S I P Y F L L F S F -
TTTTTGTATTTTTTTCTCTTTTTTACCTTTTGTCCACCATATTAAATCTTTAAACAAATCTAA
181 -----+-----+-----+-----+-----+-----+-----+ 240
AAAAACAATAAAAAGAGAAAAATGGAAAACAGTGGTATAATTTAGAAATTTGTTTAGATT
F L L F F S F Y L L S P Y * I F K Q I * -
CTATGAAAAATCCTTTAAACATATGTTAATATGTGGAAAAATAAATACTAAAATAAAAAT
241 -----+-----+-----+-----+-----+-----+-----+ 300
GATACTTTTTTAGGAAATTTGTATAACAATTATACACCTTTTATTTATGATTTTATTTTA
L * K N P L N I C * Y V E N K Y * N K N -
CTAGAACTGAAGGAAATAGTAACGGATTATTTAGGTATGATATCAGCACTAGATTCTATA
301 -----+-----+-----+-----+-----+-----+-----+ 360
GATCTTGACTTCCTTTATCATTCCTAATAAATCCATACTATAGTCGTGATCTAAGATAT
L E L K E I V T D Y L G M I S A L D S I -
CCCGAGCCCCAAAACCTTTGCGCCTAGTCCAGATTTCAAATGGCTTTGTGAAGAGCTATTT
361 -----+-----+-----+-----+-----+-----+-----+ 420
GGGCTCGGGGTTTTGAAACGCGGATCAGGTCTAAAGTTTACCGAAACACTTCTCGATAAA
P E P Q N F A P S P D F K W L C E E L F -
GTGAAGATACATGAAGTTCAAATTAATGGAACGGCCGGCACTGGCAAATCAAGGTCTTTC
421 -----+-----+-----+-----+-----+-----+-----+ 480
CACTTCTATGTACTTCAAGTTTAATTACCTTGCCGGCCGTGACCGTTTAGTTCCAGAAAG
V K I H E V Q I N G T A G T G K S R S F -
AAGTACTATGAAATAATATCGAATTTTCGTGAAATGTGGAGAAAAACCGTGGGAAATAAT
481 -----+-----+-----+-----+-----+-----+-----+ 540
TTCATGATACTTTATTATAGCTTAAAGCAGCTTTACACCTCTTTTGGCACCCCTTTATTA
K Y Y E I I S N F V E M W R K T V G N N -
ATATATCCTGCACTGGTTCTTGCTCTTCCCTACCGCGATAGACGAATCTATAATATTAAG
541 -----+-----+-----+-----+-----+-----+-----+ 600
TATATAGGACGTGACCAAGAACGAGAAGGGATGGCGCTATCTGCTTAGATATTATAATTC
I Y P A L V L A L P Y R D R R I Y N I K -



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FIG. 6 (CONT.)

601 GATTATGTATTAATAAGAACTATATGCTCTTACTTGAAGTTGCCAAAAAATTCTGCAACA
-----+-----+-----+-----+-----+-----+-----+ 660
CTAATACATAATTATTCTTGATATACGAGAATGAACTTCAACGGTTTTTTAAGACGTTGT
D Y V L I R T I C S Y L K L P K N S A T -
GAGCAGCGGTTAAAAGATTGGAAACAGCGTGTGGTAAAGGTGGGAATCTTTCTTCTCTT
661 -----+-----+-----+-----+-----+-----+ 720
CTCGTCGCCAATTTTCTAACCTTTGTGCGCACAGCCATTTCCACCCTTAGAAAGAAGAGAA
E Q R L K D W K Q R V G K G G N L S S L -
CTTGTGGAAGAAATTGCTAAAAGAAGGGCTGAACCTAGCTCAAAGCGATTACAATTGAT
721 -----+-----+-----+-----+-----+-----+ 780
GAACACCTTCTTTAACGATTTTCTTCCCGACTTGGATCGAGTTTTCGCTAATGTTAACTA
L V E E I A K R R A E P S S K A I T I D -
AACGTCAATCACTATCTGGATAGTTTGAGTGGAGACAGGTTTCGCTTCCGGACGAGGATTT
781 -----+-----+-----+-----+-----+-----+ 840
TTGCAGTTAGTGATAGACCTATCAAACCTCACCTCTGTCCAAGCGAAGGCCTGCTCCTAAA
N V N H Y L D S L S G D R F A S G R G F -
AAGAGTCTTGTCAAGTCCAAACCTTTCTGCACTGTGTGGAGAATATGAGTTTTCGTCGAA
841 -----+-----+-----+-----+-----+-----+ 900
TTCTCAGAACAGTTTCAGGTTTGGAAAGGACGTGACACACCTCTTATACTCAAAGCAGCTT
K S L V K S K P F L H C V E N M S F V E -
TTAAAATACTTCTTTTGATATCGTGTCTTAAAAATAGAGTAATAGGAGGTCAAGAGCACAAA
901 -----+-----+-----+-----+-----+-----+ 960
AATTTTATGAAGAACTATAGCACGAATTTTATCTCATTATCCTCCAGTTCTCGTGT
L K Y F F D I V L K N R V I G G Q E H K -
TTGCTAAACTGCTGGCATCCTGATGCTCAGGATTATCTTAGCGTGATATCTGATTTAAAG
961 -----+-----+-----+-----+-----+-----+ 1020
AACGATTTGACGACCGTAGGACTACGAGTCCTAATAGAATCGCACTATAGACTAAATTT
L L N C W H P D A Q D Y L S V I S D L K -
GTGGTAACTTCAAAACTTTATGATCCAAAAGTTTCGTCTAAAGGATGATGATTTGAGTATA
1021 -----+-----+-----+-----+-----+-----+ 1080
CACCATTGAAGTTTGTAAATACTAGGTTTTCAAGCAGATTTCTTACTACTAAACTCATAT
V V T S K L Y D P K V R L K D D D L S I -
AAAGTTGGCTTTGCATTCGCCCCCAATTAGCCAAAAAGTGAATCTTTCTTATGAGAAA
1081 -----+-----+-----+-----+-----+-----+ 1140
TTTCAACCGAAACGTAAGCGGGGGTTAATCGGTTTTTCACTTAGAAAGAATACTCTTT
K V G F A F A P Q L A K K V N L S Y E K -
ATATGCCGTACACTACATGATGATTTTTTGGTAGAAGAAAAAATGGATGGAGAACGAATT
1141 -----+-----+-----+-----+-----+-----+ 1200
TATACGGCATGTGATGTACTACTAAAAAACCATCTTCTTTTTTACCTACCTCTTGCTTAA
I C R T L H D D F L V E E K M D G E R I -
CAAGTTCATTATATGAATTATGGTGAATCCATAAAATTTTTTAGTAGACGGGGCATCGAC
1201 -----+-----+-----+-----+-----+-----+ 1260
GTTCAAGTAATATACTTAATACCACTTAGGTATTTTAAAAAATCATCTGCCCCGTAGCTG
Q V H Y M N Y G E S I K F F S R R G I D -



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FIG. 6 (CONT.)

1261 TATACCTATTTGTACGGAGCGAGCTTATCATCAGGAACTATATCTCAACATTTGAGGTTT 1320
-----+-----+-----+-----+-----+-----+
ATATGGATAAACATGCCTCGCTCGAATAGTAGTCCTTGATATAGAGTTGTAAACTCCAAA
Y T Y L Y G A S L S S G T I S Q H L R F -
1321 ACAGATAGTGTAAAGAATGTGTTTATAGATGGAGAAATGGTGACGTTTGATGCAAAAAGA 1380
-----+-----+-----+-----+-----+-----+
TGTCTATCACAATTTCTTACACAAAATCTACCTCTTTACCACTGCAAACTACGTTTTTCT
T D S V K E C V L D G E M V T F D A K R -
1381 CGGGTGATTCTTCCATTTCGGTCTTGTTAAAGGAAGTGCAAAGGAAGCGCTATCTTTTAAT 1440
-----+-----+-----+-----+-----+-----+
GCCCCATAAGAAGGTAAGCCAGAACAAATTTCTTCACGTTTCTTCGCGATAGAAAATTA
R V I L P F G L V K G S A K E A L S F N -
1441 AGTATAAATAATGTTGACTTTTACCCCTTATATATGGTGTTTGATCTGTTATACCTGAAT 1500
-----+-----+-----+-----+-----+-----+
TCATATTTATTACAACGTGAAAGTGGGGAATATATACCACAACTAGACAATATGGACTTA
S I N N V D F H P L Y M V F D L L Y L N -
1501 GGGACTTCGTTGACACCATTACCCCTTCATCAAAGGAAGCAATATCTGAACAGCATTTTA 1560
-----+-----+-----+-----+-----+-----+
CCCTGAAGCAACTGTGGTAATGGGGAAGTAGTTTCTTCGTTATAGACTTGTCTGTAATAAT
G T S L T P L P L H Q R K Q Y L N S I L -
1561 AGTCCCTTGAAAAATATTTGTAGAAATAGTACGATCTTCTAGATGTTATGGTGTTGGAGTCA 1620
-----+-----+-----+-----+-----+-----+
TCAGGGAACTTTTTATAACATCTTTATCATGCTAGAAGATCTACAATACCACACCTCAGT
S P L K N I V E I V R S S R C Y G V E S -
1621 ATCAAAAAGTCTTTAGAAGTTGCAATCTCACTGGGTTGAGAAGGAGTTGTTTTGAAATAT 1680
-----+-----+-----+-----+-----+-----+
TAGTTTTTCAGAAATCTTCAACGTTAGAGTGACCCAAGTCTTCTCAACAAAACCTTTATA
I K K S L E V A I S L G S E G V V L K Y -
1681 TATAATTCAAGTTATAATGTGCGCCAGTCGAAACAACAACCTGGATCAAGGTAAAACCTGAA 1740
-----+-----+-----+-----+-----+-----+
ATATTAAGTTCAATATTACAGCGGTCAGCTTTGTTGTTGACCTAGTTCCATTTTGGACTT
Y N S S Y N V A S R N N N W I K V K P E -
1741 TATTTGGAGGAATTTGGAGAGAATTTAGACTTAATAGTAATAGGCAGAGATTCTGGGAAA 1800
-----+-----+-----+-----+-----+-----+
ATAAACCTCCTTAAACCTCTCTTAAATCTGAATTATCATTATCCGTCTCTAAGACCCCTT
Y L E E F G E N L D L I V I G R D S G K -
1801 AAAGATTCTTTTATGCTAGGGTTACTTGTGCTAGATGAAGAAGAGTATAAAAAGCACCAA 1860
-----+-----+-----+-----+-----+-----+
TTTCTAAGAAAATACGATCCCAATGAACACGATCTACTTCTTCTCATATTTTTCGTGGTT
K D S F M L G L L V L D E E E Y K K H Q -
1861 GGAGACTCCTCTGAAATTGTAGACCACTCAAGCCAAGAAAAACACATACAAAATTCAAGA 1920
-----+-----+-----+-----+-----+-----+
CCTCTGAGGAGACTTTAACATCTGGTGAGTTCGGTCTTTTTTGTGTATGTTTTAAGTTCT
G D S S E I V D H S S Q E K H I Q N S R -
AGAAGGGTGAAAAAATACTTTTCACTTCTGTTCTATCGCAACCGGTATATCTCAAGAAGAA



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FIG. 6 (CONT.)

1921 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 1980
TCTTCCCACCTTTTATGAAAGTAAGACAAGATAGCGTTTGCCATATAGAGTTCTTCTT
R R V K K I L S F C S I A N G I S Q E E -
TTCAAAGAAATCGACCGCAAAACGAGAGGACATTGGAAAAGAACCTCCGAAGTTGCTCCC
1981 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2040
AAGTTTCTTTAGCTGGCGTTTGTCTCTCTGTAACCTTTTCTTGGAGGCTTCAACGAGGG
F K E I D R K T R G H W K R T S E V A P -
CCTGCTTCAATTTTGAATTTGGCTCAAAAATACCTGCCGAATGGATTGACCCCAAGTGAA
2041 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2100
GGACGAAGTTAAATCTTAAACCGAGTTTATGGACGGCTTACCTAACTGGGGTCACTT
P A S I L E F G S K I P A E W I D P S E -
TCAATTGTTCTAGAAATAAAATCACGGTCTTTGGATAACACAGAAACGAATATGCAGAAG
2101 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2160
AGTTAACAAGATCTTTATTTTAGTGCCAGAAACCTATTGTGTCTTTGCTTATACGTCTTC
S I V L E I K S R S L D N T E T N M Q K -
TACGCTACCAATTGTACTTTGTACGGTGGCTATTGTAAAAGAATACGGTACGATAAAGAA
2161 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2220
ATGCGATGGTTAACATGAAACATGCCACCGATAACATTTTCTTATGCCATGCTATTTCTT
Y A T N C T L Y G G Y C K R I R Y D K E -
TGGACAGATTGTTACACACTTAACGACTTATACGAAAGTAGGACGGTTAAATCTAACCCC
2221 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2280
ACCTGTCTAACAATGTGTGAATTGCTGAATATGCTTTCATCCTGCCAATTTAGATTGGGG
W T D C Y T L N D L Y E S R T V K S N P -
AGCTATCAAGCGGAAAGGTCACAGCTTGGATTGATACGGAAAAAGAGAAAGAGTACTT
2281 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2340
TCGATAGTTGCGCTTTCCAGTGTGGAACCTAACTATGCCTTTTCTCTTTCTCTCATGAA
S Y Q A E R S Q L G L I R K K R K R V L -
ATTTACAGACAGCTTTCACCAAAACAGGAAACAACCTGCCAATTTCAAACATCTTTGCCGGA
2341 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2400
TAAAGTCTGTGGAAGTGGTTTGTCTCTTGTGACGGTTAAAGTTGTAGAAACGGCCT
I S D S F H Q N R K Q L P I S N I F A G -
TTACTTTTATGTTCTCTCTGACTATGTACGGAGGACACTGGAATACGGATTACACGG
2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
AATGAAAAAATACAAGAGAGACTGATACAGTGCTCCTGTGACCTTATGCCTAATGTGCC
L L F Y V L S D Y V T E D T G I R I T R -
GCAGAACTTGAAAAAACTATTGTGGAACATGGTGGTAAACTGATATATAATGTAATTTTA
2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
CGTCTTGAACCTTTTGTGATAACACCTTGTACCACCATTTGACTATATATTACATTAAAT
A E L E K T I V E H G G K L I Y N V I L -
AAACGTCATTCAATTGGGGACGTTGGTTAATCAGCTGTAAAACTACCACGGAATGCAAG
2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
TTTGCAGTAAGTTAACCCTGCAAGCCAATTAGTCGACATTTTGTATGGTGCCTTACGTT
K R H S I G D V R L I S C K T T T E C K -
GCTTTAATAGATCGAGGATATGATATATTGCACCCAAATGGGTACTCGATTGTATAGCA
2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640



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FIG. 6 (CONT.)

CGAAATTATCTAGCTCCTATACTATATAACGTGGGTTTAACCCATGAGCTAACATATCGT
A L I D R G Y D I L H P N W V L D C I A -
TATAAGAGGCTCATCTGATCGAGCCCAATTATGTCTTTAACGTCTCTCAAAAAATGAGA
2641 -----+-----+-----+-----+-----+ 2700
ATATTCTCCGAGTAGGACTAGCTCGGGTTAATAACGAAATTGCAGAGAGTTTTTTTACTCT
Y K R L I L I E P N Y C F N V S Q K M R -
GCCGTCGCTGAAAAAAGGGTAGATTGTTTGGGTGATAGTTTTTGAAAATGACATTTTCGGAA
2701 -----+-----+-----+-----+-----+ 2760
CGGCAGCGACTTTTTTCCCATCTAACAAACCCACTATCAAAACTTTTACTGTAAAGCCTT
A V A E K R V D C L G D S F E N D I S E -
ACCAAACTGTCATCATTTGTATAAATCACAACTAAGTCTACCACCGATGGGGGAACTCGAG
2761 -----+-----+-----+-----+-----+ 2820
TGGTTTGACAGTAGTAACATATTTAGTGTGATTGATGATGGTGGCTACCCCCCTGAGCTC
T K L S S L Y K S Q L S L P P M G E L E -
ATAGATTCTGAGGTTCCGGCGGTTTCCATTATTTTTATTCTCCAACAGGATTGCATACGTA
2821 -----+-----+-----+-----+-----+ 2880
TATCTAAGACTCCAAGCCGCCAAAGGTAATAAAAATAAGAGGTTGTCCTAACGTATGCAT
I D S E V R R F P L F L F S N R I A Y V -
CCACGTCGCAAAATTAGCACAGAAGATGACATTATAGAAATGAAAATTAAGTTGTTTGGT
2881 -----+-----+-----+-----+-----+ 2940
GGTGCAGCGTTTTAATCGTGTCTTCTACTGTAATATCTTTACTTTTAATTCAACAAACCA
P R R K I S T E D D I I E M K I K L F G -
GGAAAAATAACAGATCAACAGTCACTTTGTAACCTAATAATTATACCATATACTGATCCT
2941 -----+-----+-----+-----+-----+ 3000
CCTTTTTATTGTCTAGTTGTGTCAGTGAAACATGAATTATTAATATGGTATATGACTAGGA
G K I T D Q Q S L C N L I I I P Y T D P -
ATTTTGAGGAAAGACTGCATGAATGAGGTACACGAAAAATAAAAGAACAAATAAAGGCT
3001 -----+-----+-----+-----+-----+ 3060
TAAAACTCCTTTCTGACGTACTTACTCCATGTGCTTTTTTATTTTCTTGTTTATTTCCGA
I L R K D C M N E V H E K I K E Q I K A -
TCTGATACTATACCGAAAAATAGCCAGGGTCGTTGCCCTGAATGGGTGGATCATTCTATT
3061 -----+-----+-----+-----+-----+ 3120
AGACTATGATATGGCTTTTATCGGTCCCAGCAACGGGGACTTACCCACCTAGTAAGATAA
S D T I P K I A R V V A P E W V D H S I -
AATGAAAACCTGTCAAGTGCCTGAAGAAGACTTCCCCGTAGTCAACTACTGATGGTGGCTT
3121 -----+-----+-----+-----+-----+ 3180
TTACTTTTGACAGTTCACGGACTTCTTCTGAAGGGGCATCAGTTGATGACTACCACGCAA
N E N C Q V P E E D F P V V N Y * W C V -
TTGCGGAGGCTTAATTTTTTTGAAGTTTATTTAATACTATCCTACATATGTACATTAAATA
3181 -----+-----+-----+-----+-----+ 3240
AACGCCTCCGAATTAAAAAAGCTTCAAATAAATTATGATAGGATGTATACATGTAATTTAT
L R R L N F L K F I * Y Y P T Y V H * I -
CTTCGGTAAACGTTTATCAATAAGAGTGGGAAGATGGCAATTATATTCAAAGATTGGCCA
3241 -----+-----+-----+-----+-----+ 3300
GAAGGCATTGCAAAATAGTTATTCTCACCTTCTACGGTTAATATAAGTTTTCTAACCGGT



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FIG. 6 (CONT.)

L P * R L S I R V E D A Q L Y S K D W P -

3301 GTCAATTAACTTAAGGAAAAAAT
-----+-----+--- 3323
CAGTTAATTGAATTCCTTTTITA

V N * L K E K